

GENETIC DIVERSITY IN LAND RACES OF RIDGE GOURD

A.K.M. Quamruzzaman^{*1}, M. H.Rahman¹, Md. Nazrul Islam¹, S.M. L. Rahman² and B.C. Sarker³

ABSTRACT

The genetic divergence among thirty genotypes of ridge gourd (*Luffa acutangula*) was estimated using D^2 and principal component analysis. The genotypes were grouped into six clusters. The clustering pattern of the genotypes showed high degree of genetic diversity. The highest intra-cluster distance was noticed for the cluster II (0.882) and the lowest for the cluster III (0.220). The highest inter-cluster distance was observed between cluster I and II (15.045) where as the lowest was observed between cluster IV and V (3.402). Selection for days to 1st male flower open, days to 1st female flower open, fruit diameter, single fruit weight and fruit number/plant would be more effective for increasing qualitative yield of ridge gourd. On the basis of the present study, suggestions has been made for selecting parents so as to initiate a crossing programme to produce new recombinants with desired characters in ridge gourd.

Key word: Genetic diversity, ridge gourd (*Luffa acutangula*) and cluster.

Introduction

Ridge gourd (*Luffa acutangula*) is one of the most important summer vegetable in Bangladesh. It belongs to the botanical family cucurbitaceae. The national yield average is being only 6.67 t/ha (Anon. 2005), which is very low. Ridge gourd is very nutritious due to its high content of vitamin A. In Bangladesh ridge gourd can play a vital role in alleviating malnutrition.

Information on genetic divergence among the plant materials is vital to a plant breeder for an efficient choice of parents for hybridization. It is an established fact that genetically diverse parents are likely to contribute desirable segregants and or to produce high heterotic crosses. More diverse the parents greater are the chances of obtaining high heterotic F_1 s and broad spectrum of variability in segregating generations (Murty and Arunachalam 1966). Improvement in yield and quality is normally achieved by selecting genotypes with desired character combinations existing in the nature or by hybridization. The parents identified on the basis of

^{*}Corresponding Author

¹ Horticultural Research Centre, Bangladesh Agricultural Research Institute (BARI), Gazipur-1701
Authors email: akmqzs@gmail.com,

²Citrus Research Station, BARI, Jaintapur, Sylhet,

³ Regional Agricultural Research Station, BARI, Jamalpur, Bangladesh

divergence analysis would be more promising. In both cross and self pollinated crops genetic diversity is one of the most important tools to quantify genetic variability (Griffing and Lindstrom 1954, Murty and Arunachalam 1966, Gaur *et al.* 1978). The qualification of genetic diversity through biometrical procedures has made it possible to choose genetically diverse parents for a successful hybridization program (Rao 1952 and Jain *et al.* 1975). Tomooka (1991) also reported that evaluation of genetic diversity is important to know the source of gene for a particular trait within the available germplasm. The investigation was undertaken with 30 local ridge gourd genotypes. In Bangladesh, the information on this aspect of ridge gourd is scarce. The paper described the nature and magnitude of genetic diversity of ridge gourd genotypes.

Materials and Methods

The experiment was conducted at the farm of Olericulture Division, HRC, BARI, Gazipur, during the summer season of 2005. The seeds were sown in the polybag on 01 March 2006 and 20 days old seedlings were transplanted in the main field on 20 March 2005. The experiment was laid out in RCB design with three replications. The unit plot size was 7.5 x 1.25m. The land was fertilized with cow dung, urea, TSP, MP, gypsum and zinc @ 20000, 175, 175, 150, 100 and 12 kg/ha, respectively. The total amount of cow dung, TSP, gypsum and zinc and 1/3rd of each of urea and MP were applied during final land preparation and in the pit. The rest of urea and MP were applied in four equal installments at 21, 35, 55 and 75 days after transplanting. The seedlings were transplanted to the main plot maintaining 1.5 x 1.25m spacing. The intercultural operations were done as and when needed. Data on days to 1st male flower open, days to 1st female flower open, node order to 1st male flower open, node order to 1st female flower open, fruit length (cm), fruit diameter (cm), single fruit weight (g), fruit number/ plant, harvest duration (days) and yield/ plant (kg) were recorded from three randomly selected plants per entry per replication. Genetic diversity was estimated following Mahalanobis's (1936) generalized distance (D^2) extended by Rao (1952). Tocher's method (Rao 1952) was followed for determining the group constellations. Canonical analysis was also done according to Rao (1964) to confirm the results of cluster and D^2 analysis. Based on D^2 values, the thirty genotypes were grouped into clusters using the Genstat 5 computer software.

Results and Discussion

The analysis of variance revealed significant variations among the genotypes of ridge gourd for all the characters studied. The D^2 values ranged from 3.402-

15.0445 (Table 2) and principal component scores (Table 4) also indicated a high degree of genetic diversity among the genotypes.

Table 1. Distribution of thirty genotypes of ridge gourd in six clusters

Clusters	Number of genotypes	Genotypes
I	2	RGN16, RGN20
II	4	RGN09, RGN10, RGN11, RGN21
III	2	RGN03, RGN12
IV	9	RGN05, RGN06, RGN07, RGN08, RGN13, RGN17, RGN18, RGN27, RGN29
V	5	RGN01, RGN02, RGN22, RGN23, RGN30
VI	8	RGN04, RGN14, RGN15, RGN19, RGN24, RGN25, RGN26, RGN28

Thirty genotypes were grouped into six clusters. Cluster IV was consisted of maximum nine genotypes, followed by cluster VI with eight genotypes, cluster V and II with five and four genotypes respectively. While cluster I and III was consisted of two genotype each (Table 1.). Highest inter cluster distance was observed between cluster I and II (15.045) followed by cluster I and VI (11.960) and cluster I and IV (11.372). Genotypes belonging to the clusters with maximum intercluster distance is genetically more diverged. Selection of parents for hybridization should be chosen from two clusters having wider intercluster distance to get more variability. The genotypes RGN16, RGN20 from cluster I and genotypes RGN09, RGN10, RGN11, RGN21 from cluster II are the best choice for hybridization. The minimum intercluster divergence was observed between cluster IV and V (3.402) and cluster IV and VI (3.497), indicating that the genotypes of these clusters were genetically closed. The intra-cluster divergence varied from 0.220 to 0.882. The highest value being in cluster II, while lowest value in cluster III (Table 2.).

Table 2. Mean intra (bold) and inter cluster distances (D^2) for the thirty ridge gourd genotypes obtained on the basis of ten morphological characters.

Clusters	I	II	III	IV	V	VI
I	0.542	15.045	10.669	11.372	10.927	11.960
II		0.882	10.969	10.741	9.504	7.997
III			0.220	9.487	7.250	9.016
IV				0.467	3.402	3.497
V					0.397	3.529
VI						0.563

Differences in cluster means existed for almost all the characters (Table 3). Cluster I comprising of two genotypes (RGN16, RGN20). The mean values of this cluster ranked first for fruit length (23 cm), fruit number/ plant (26) and yield/ plant

(9.7kg) and second for single fruit weight (127g) (Table 3). Whereas minimum mean values was not found in this cluster. Cluster mean for yield/ plant was the highest which might be due to the maximum fruit number/ plant and second highest value for single fruit weight. Prasad *et al.* (1993) also reported the similar findings relating to fruit bearing in cucumber.

Cluster II comprising of four genotypes (RGN09, RGN10, RGN11, RGN21) and had the highest cluster mean value for days to 1st female flower open (75.0), node order to 1st male flower open (22.0) and node order to 1st female flower open (46.0). But these higher mean values are not desirable for earliness. Whereas the lowest cluster mean value for fruit diameter (3.3cm), fruit number/ plant (18.0), harvest duration (48.0days) and yield/ plant (1.7kg)

Cluster III comprising of two genotypes (RGN03, RGN12) and ranked first in respect of cluster mean values for fruit diameter (3.8cm) and harvest duration (64.0days) and second highest mean values for fruit number/ plant (43.0). The minimum mean values was observed in days to 1st female flower open (60.0 days), node order to 1st female flower open (27.0), fruit length (13.0cm) and single fruit weight (85.0g). Minimum mean values for days to 1st female flower open and node order to 1st female flower open is desirable for earliness.

The cluster IV was comprising of nine genotypes (RGN05, RGN06, RGN07, RGN08, RGN13, RGN17, RGN18, RGN27, RGN29) had highest cluster mean values for days to 1st male flower open (56.0 days) and single fruit weight (141.0g) and second highest mean values for fruit length (22.0cm), fruit diameter (3.7cm), harvest duration (60.0days) and yield/ plant (3.9kg). The cluster IV failed to show the lowest mean values for none of the ten characters.

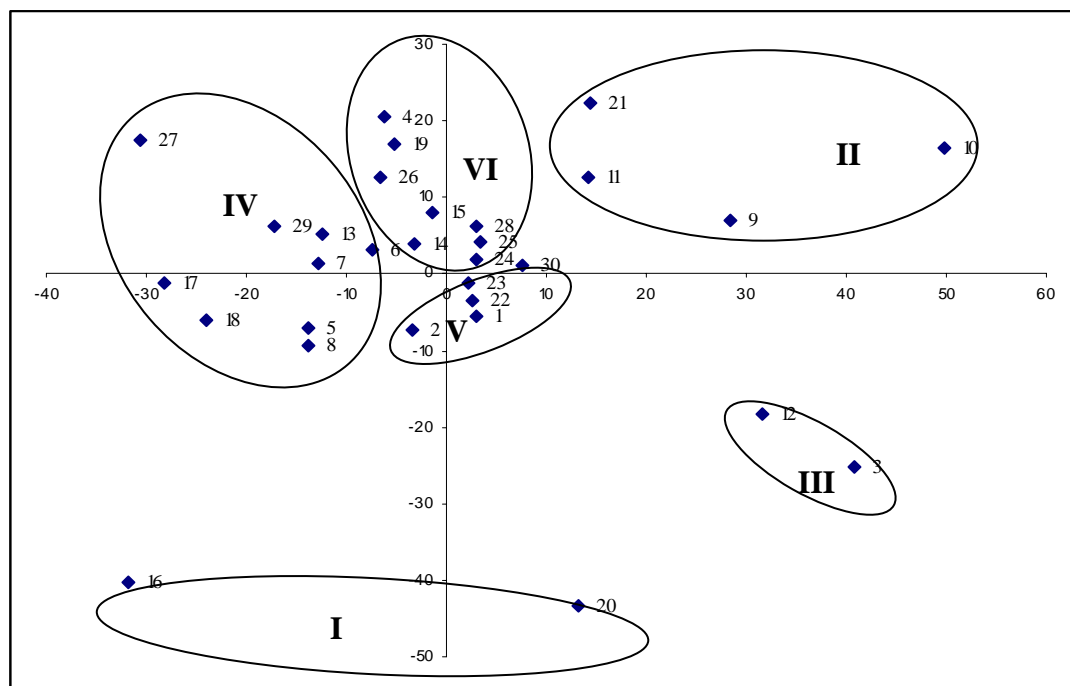
Five genotypes (RGN01, RGN02, RGN22, RGN23, RGN30) were in cluster V which had highest cluster mean values for only node order to 1st male flower open (16.5) which was not a desirable trait for early fruiting. No lowest mean value was obtained in this cluster.

The cluster VI comprising of eight genotypes (RGN04, RGN14, RGN15, RGN19, RGN24, RGN25, RGN26, RGN28) and failed to show any highest mean values for none of the ten characters. Days to 1st male flower open (62.0 days) was maximum among the entire cluster.

Table 3. Cluster means for 10 characters in 30 genotypes of ridge gourd

Characters	Clusters					
	I	II	III	IV	V	VI
Days to 1 st male flower open	57.0	61.0	57.0	56.0	57.0	62.0
Days to 1 st female flower open	66.0	75.0	60.0	65.0	63.0	70.0
Node order to 1 st male flower open	18.0	22.0	20.0	18.0	16.5	21.0
Node order to 1 st female flower open	28.0	46.0	27.0	31.0	28.0	31.0
Fruit length (cm)	23.0	19.0	13.0	22.0	19.0	21.0
Fruit diameter (cm)	3.5	3.3	3.8	3.7	3.6	3.5
Single fruit weight (g)	127.0	93.0	85.0	141.0	120.0	124.0
Fruit number/ plant	76.0	18.0	43.0	27.0	28.0	22.0
Harvest duration (days)	55.0	48.0	64.0	60.0	59.0	49.0
Yield/ plant (kg)	9.7	1.7	3.7	3.9	3.4	2.8

Based on principal component axes I and II, a two-dimensional scattered plotting diagram (Z_1 and Z_2) of the genotypes are presented in Figure 1, reflecting the position of genotypes. The scattered diagram revealed that apparently there were mainly six clusters. Distantly located genotypes of different clusters were RGN16, RGN20 in cluster I and RGN09, RGN10, RGN11, RGN21 in cluster II. Pattern of distribution of genotypes in the scattered diagram revealed that considerable variability exist in the genotypes.

**Fig 1.** Scatter distribution of 30 ridge gourd genotypes on principal component score superimposed with clustering

The results of PCA revealed that in vector 1 (Z₁) the important characters responsible for genetic divergence in major axis of differentiation were days to 1st male flower open (0.0034), days to 1st female flower open (0.0552), fruit diameter (1.1237), single fruit weight (0.1121) and fruit number/ plant (0.3774). In vector 2 (Z₂) days to 1st male flower open (0.0218), days to 1st female flower open (0.1151), fruit diameter (0.7453), single fruit weight (0.2030), fruit number/ plant (0.2086) and harvest duration (0.0251) played a major role while the rest of the characters played a minor role in the second axis of differentiation. The role of days to 1st male flower open, days to 1st female flower open, fruit diameter, single fruit weight and fruit number/ plant, in the both vectors indicated their importance in genetic divergence. Alam *et al.* (2006) reported that days to heading, 1000 grain weight, yield/ plant were the major contributors towards divergence in hull-less barley. Masud *et al.* (1995) found that number of fruits per plant and yield per plant was one of the important contributors to genetic divergence in pumpkin. Moreover Habib *et al.* (2007) in rice reported same result for grain/ panicle, grain length and harvest index.

Table 4. Latent vectors for 10 quantitative characters of 30 genotypes of ridge gourd

Characters	Vector (Z ₁)	Vector (Z ₂)
Days to 1 st male flower open	0.0034	0.0218
Days to 1 st female flower open	0.0552	0.1151
Node order to 1 st male flower open	-0.1426	-0.2027
Node order to 1 st female flower open	-0.1111	-0.1313
Fruit length (cm)	-0.1818	-0.0316
Fruit diameter (cm)	1.1237	0.7453
Single fruit weight (g)	0.1121	0.2030
Fruit number/ plant	0.3774	0.2086
Harvest duration (days)	-0.0015	0.0251
Yield/ plant (kg)	-1.5463	-2.5731

The clustering pattern of D² analysis in table (Table 1) has followed the same trend of distribution of genotypes in PCA. The D² and PCA were found to be an alternative method in giving the information regarding the clustering pattern. Moreover, the PCA provides information on contribution of the characters towards divergence.

The crosses involving parents belonging to the maximum divergent clusters were expected to manifest maximum heterosis and also wide variability in genetic architecture. Ramanujam *et al.* (1974) in mung bean and Mian and Bhal (1989) in chick

pea reported that parental clusters separated by medium D^2 values exhibited significant and positive heterosis for seed yield and some of its components in mung bean. Thus crosses between the genotypes of cluster I with that of cluster II, cluster I with cluster III and cluster I with cluster IV would exhibit high heterosis and is also likely to produce new recombinants with desired characters in ridge gourd. Hence, considerable emphasis should be given on these characters to increase qualitative yield of ridge gourd. Mathew *et al.* (1986) reported that fruits per plant and fruit weight were the major contributors towards divergence in *Cucumis melo*.

The genetic diversity should be utilized for the development of gene pools, which serve as the reservoirs of genes. Information on genetic diversity can also be utilized for the exploitation of hybrid vigor.

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